Gédigi erwinia car Q7u4vo synechococc Q8196 bacillus ch Q731ro bacillus ce Q81mj bacillus an A843007 bacillus an A843374 bacillus A8493 pseudomonas O67788 aquifex aeo Q86x3 leptospira Q7552 leptospira

us-10-629-329a-2.rup

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AVMATLLFPGREFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHA 180
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Lidentification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000)
EMBL; AR132963; AAD27738011; -.
InterPro; IPR001303; Aldolase_II. N.
Pfam; PF00596; Aldolase_II. 1.
SEQUENCE 242 AA; 27012 MW; 7B99194024C77D5B CRC64;
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07V8Y6
06D1G1
06D1G1
07V8V0
0819E6
0731R0
0731R0
081M70
081M70
081W79
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity 99.6
Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
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Q96kx2 homo sapien
Q96kx2 homo sapien
Q96xq5 mus musculu
Q60x23 xenopus lae
Aah6873 xenopus lae
Aah6873 xenopus lae
Aah10131 homo sapien
Aah10131 homo sapien
Q7p32 homo sapien
Q7p32 anopheles g
Q6cbb yarrowia li
Q9fn41 arabidopsis
Aa1042 arabidopsis
Aa1042 sarabidopsis
Aa1042 sarabidopsis
Aa1052 asacharomyc
Q55p5 ashbya goss
Aa51102 ashbya goss
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   (without alignments)
   696.203 Million cell updates/sec
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                      5.1.6
Compugen Ltd
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                      GenCore version (c) 1993 - 2005
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09VY33
09VY33
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07PS25
07BS25
06CBB0
09FN41
AAT06425
07S746
06BIX5
VGA YEAST
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Q9UT22
MTNB BACSU
Q828L0
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Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Q96GX9
Q98WVU2
Q9WVQ5
Q9WVQ5
Q6NU29
AAH68773
Q6PJX6
AAH10133
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Q23261
Q6CM29
Q9HE08
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Maximum DB seq
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RA Attacher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Attacher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Attacher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Attacher B. B. Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Baconstein M.J., Usdin T.B., Toshiyuki S., Carninol E., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nitlalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
R Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
A Jones S.J., Marra M.A.;
The mouse cDNA sequences.",
R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 2.7e-109;
0; Mismatches 2; Indels (
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009077; AAH09077.1; -.
InterPro; IRRO01303; Aldolase_II_N.
Pfan; PF00596; Aldolase_II; I.
SEQUENCE 242 AA; 27125 MW; 9BBD5D1435D6775A CRC64;
 Last sequence update)
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Last sequence update)
                                                                                                                                             MEDLINE=22388257; PubMed=12477932;
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Best Local Similarity 99.2%;
Matches 240; Conservative
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  01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
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                                                    Homo sapiens (Human)
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                             CGI-29 protein.
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01-MAR-2002
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Q8WVU2;
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NEDLINE=20288257; PubMed=12477932;

NEDLINE=22388257; PubMed=12477932;

Atlausner R.D., Celling F.S., Wagner L., Schaefer C.E., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Antenenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bromstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bromstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bromstein M.J., Wokernan R.J., Maruson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
A Gones S.J., Marra M.A.,
Todenezation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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98.8%; Pred. No. 2.6e-108;
ive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
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Matches 239; Conservative
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(TrEMBLrel.
                                                     Name=MMRP19;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001
01-DEC-2001
01-MAR-2002
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ID 099
AC 099
DT 011
DT 011
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STATAIS-C57BL/6J; TISSUE=Manmary gland;
MEDLINE=22388257; PubMed=12477931.
A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A trausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A trausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A trausberg R.D., Oordan H., Moore T., Max S.I., Wang J., Haishe F.,
A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B capleron M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
A praperon M.J., Usdin T.B., Tooshiyuki S., Carainci P., Prange C.,
B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Brownstein M.J., McKerran K.J., Malke J.A., Gunzarane P.H.,
A Brask S.A., McZwan P.J., McKerran K.J., Malke J.A., Gunzarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Schiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.,
A Marra M.A., Schalbka U., Smailus D.E., Schnerch A., Schein J.E.,
A Marra M.A.,
A Marr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKA
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                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 241;
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93.8%; Pred. No. 3.2e-103;
ive 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sha S., Aoki Y., Nishi Y.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
Name=Mmrp19; Synonyms=MMR19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."
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                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=10090,
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Q8BP46
ID Q8BP46
셤
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                                                                                                                                                                                                                                       TISSUE-Bone marrow,

WEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MALtschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

MALtschul S.F., Joedan H., Moore T., Max S.I., Wang J., Heieh F.,

MALTSCHUL S.F., Joedan H., Moore T., Max S.I., Wang J., Heieh F.,

MALTSCHUL S.F., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MALTSCHUL S.A., McKennan K.J., Marman R.D., Mullahy S.J.,

MALTSCHUL S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MILLION D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe S.J., Helton B., Ketteman M., Madan A.M., Rottigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

MALTSCHUL S., Marra M.A.,

MALTSCHUL S., Marra M.A.,

MALTSCHUL S., Schhutz J., Myers R.M., Butterfield Y.S.,

MALTSCHUL S., Marra M.A.,

MALTSCHUL S., Scheit D.E., Schherch A., Schein J.E.,

MALTSCHUL S., Marra M.A.,

MARTACH S., MARTACH S.,

MARTACH
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                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC008440; AAH08440.1; Interpro; IRR01303; Aldolase_II_N. Pf00596; Aldolase_II_N. SEQUENCE 242 AA; 271I2 MW; 691C60447B723C1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WVQS PRELIMINARY; PRT; 241 AA. Q9WVQS; C1 NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2004 (TrEMBLrel. 28, Last annotation update) MMRP19 (CDNA sequence AB028863).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                         Bapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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IV 242
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A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., A Fukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T., A Hayashida K., Ishii Y., Itoh M., Kagawa T., Kanukawa T., Katoh H., Kawai J., Kojini Y., Itoh M., Kagawa T., Kanukawa T., Katoh H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nomira K., Nomura K., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinaka A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Tayawa A., Tayawa A., Takaku-Akahira S., Takeda Y., Tanaka T., Tagami M., A Tagawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (Apr-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AK077705; BAC36968.1; -.
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SEQUENCE FROM N.A.
STRAIN=C57BL/G17 IISSUE=Whole body;
MEDLINE=C57BL/G17 IISSUE=Whole body;
MEDLINE=2014; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730540M11 product:monocyte macrophage 19, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:553-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CSTBL/6J, TISSUE=Whole body;
MEDLINE=CSTBL/6J, TISSUE=Whole body;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MISHI N., Ishii Y., Nakamura K., Ritsunai T., Tashiro H., Itch M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshikai M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Muramateu M., Inoue Y., Kira A., Haysshizaki Y., Rutigerated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                           Mus muscúlus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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MEDLINE=99279253; PubMed=10349636;
Carninot P., Hayashizaki Y.;
Hayashizaki Y.;
Meliah-eficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN-CSTBL/6J; TISSUE-Whole body;
WEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
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                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                             Name=Mmrp19;
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TISSUE=Embryo;

RA MEDLINE=2288557; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Studin G.M., Hong L.,

RA Boaleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

RA Ana S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boak S.A., Morbay D.W., Scdergren E.J., Lu X., Glibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

RA Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Miting M., Madan A., Young A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

R. "Generation and initial analysis of more than 15,000 full-length human
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                   DB 2; Length 241;
                                                                                                                                         Indels
                   InterPro; IPR001303; Aldolase_II_N.
Pfam; PF00596; Aldolase_II; 1.
SEQUENCE 241 AA; 26933 MW; 5EC51C07E6F0D656 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                 93.0%; Score 1229.5; DB 2; 93.4%; Pred. No. 2.5e-102; ive 9; Mismatches 6;
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MGD; MGI:1926788; Mmrp19
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Name=MGC81295;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical aevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Richardson P.,
Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                   Klein S., Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                 EMBL; BC068773; AAH68773.1; -.
InterPro; IPR001303; Aldolase II N.
Pfam; PF00596; Aldolase II; 1.
SEQUENCE 239 AA; 27172 MW; 690BBAE5755AA0CB CRC64;
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NCBI_TaxID=8355;
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                                                                      Dyn. 225:384-391 (2002)
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TISSUE=FIACENTA;

RA MEDLINE=23388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeoberg B., Bouslow M.F., Rubin G.M., Hong L.,

Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratene P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rainards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rillalon D.K., Muzny D.M., Soderzen E.J., Lu X., Gibbs R.A.,

Villalon D.K., Mazny D.M., Soderzen E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rayminski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

"The stranger of the sequences.";
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., BlakeBley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skellska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 DCCSRRCGAQDKEHPRYLIPELCKQFYHLGWVTGTGGGISLKHGDEIYIAPSGVQKERIQ
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Hymo sapiens (Hyman).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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239 AA; 27172 MW; 690DBAE5755AA0CB CRC64;
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Last annotation update)
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Klein S., Strausherg R.;
Submitted (APR-2004) to the I
EMBL; BC068773; AAH68773.1;
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jest Local Similarity 62.04
Matches 191; Conservative
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234 LPVGENGIV 242
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Matches 152; Conserv
                                                              Query Match
Best Local Similarity
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05-JUL-2004
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Q9H528
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhate N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhate N.K.,
An Eschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhate N.K.,
An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
An Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Richards R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Gones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                76 IHTHSKAAVMATLLFPGREFKITHQEMIKGIKKCTSGGYYKYDDMLVVPIIENTPEEKDL 135
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                      Length 204;
                                                                                                                                                                                                 1; Indels
                                                        Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-31), AAH10133.1; -. InterPro; IPR001303; Aldolase_II_N. Pfam; PR00596; Aldolase_II; 1. Hypothetical protein: SEQUENCE 204 AA; 22858 MW; 82FC4E97BC6C2853 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                  Query Match 76.0%; Score 1005; DB 2; Best Local Similarity 99.5%; Pred. No. 3.3e-82; Matches 188; Conservative 0; Mismatches 1;
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TISSUE-Placenta;
MEDLINE-22388257; PubMed=12477932;
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                               SEQUENCE FROM N.A.
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                                              TISSUE=Placenta;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               Score 1005; DB 2; Length 204;
Pred. No. 3.3e-82;
0; Mismatches 1; Indels C
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC010133, AAH10133.1; -.
Hypothetical protein.
SEQUENCE 204 AA; 22858 MW; 82FC4E97BC6C2853 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 AA; 16918 MW; D88A0ADE331E12EA CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 21, Last annotation update)
01-791.0 2 (Similar to CGI-29 protein) (Fragment).
Name=011791.0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.8%; Score 830; DB 2; ilarity 99.3%; Pred. No. 1.3e-66; Conservative 0; Mismatches 1;
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InterPro; IPR001303; Aldolase_II_N.
Pfam; PF00596; Aldolase_II; 1.
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                                                                                                   76.0%;
99.5%;
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Matches 188; Conservative
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Celniker S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirsks R., Tabor P.E., Wan K., Stapleron M., Sutron G.G., Venter C., Weinscock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fridse E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
CG11134-PA (RE61993p).
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                                                                                                                             SEQUENCE FROM N.A.
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             ORFNames=CG11134;
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141
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Kusso S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                       "Annotation of the Drosophila melanogaster euchromatic genome:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR001303; Aldolase_II_N.
Pfam; PF00596; Aldolase_II; 1_.
SEQUENCE 227 AA; 26011 MW; 7F2E505906CE155D CRC64;
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Last annotation update)
                                                                                                                                                                                                                                             Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 AA
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Anopheles Genome Sequencing Consortium;
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01-MAR-2004 (TrEMBLrel. 26, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003493; AAF48310.1; -. EMBL; AY071553; AAL49175.1; -.
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Search completed: February 1, 2005, 14:29:28
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                                            215 AVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 VIHTHSPAAVMTTLLWPGKEFRCTHLEMIKGIYDYELNRNLMYDEELVVPIIENTLFEKD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTWCECYDXLFDIAVSMKKVGLDPS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                      EHPRYLIPELCKOFYHLGWVTGTGGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEK
                                                                                                                                                                                                                          DISGPSPSKKLKKSQCTPLFMNAYTWRGAGAVIHTHSKAAVMATLLFPGREFKITHQEMI
                                                                                                                                                                                                                                                                        KGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 GDEIYIAPSGVOKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTMRGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GDEIYIAPSGVQKERIQPDDLFIQNIEGDDLQTPPDYKKITKSQCTPLFMLAYKERSAGA
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles Genome Sequencing Consortium, Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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         CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                             Length 277;
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                                                                                                                                                   41; Indels
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                      277 AA; 30799 MW; F7F222B46EAD1F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 AA; 25086 MW; 38AD45AE255F3044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Q7PG25 PRELIMINARY; PRT; 220 AA. Q7PG25; Q10-MAR-2004 (TrEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                           50.8%; Score 671; DB 2;
68.3%; Pred. No. 5.4e-52;
iive 19; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AAABO1008845; EAA45094.1; -.
InterPro; IPR001303; Aldolase_II_N.
Pfam; PF00596; Aldolase_II; 1.
                                        EMBL; AAABO100846; EAA06311.2; -.
InterPro; IPR001303; Aldolase_II_N.
Pfam, PF00596; Aldolase_II; 1.
NON_TER 277 277 277
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                                                                                                                                                   Matches 129; Conservative
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                                  preliminary data.
                                                                                                                                         Local Similarity
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Despons L., Fabre E., Fairhead C., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
Swennene D., Tekaia F., Wesolowski-Louvel M. Westhof E., Wirth B.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.,
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                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to spl P47095 Saccharomyces cerevisiae YJR024c.
ORFNames=YALI0C204279;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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SEQUENCE 238 AA; 26590 MW; B63E556136278CE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 YVWGETVWKAKVYNEAIDYLLELAVKMIQMGIDP-----EGGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 54.59
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 430:35-44(2004).
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SEQUENCE FROM N.A.
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